

## AMENDMENTS

### In the specification:

Please replace the paragraph beginning at page 19, line 15 with the following paragraph:

In a particularly preferred embodiment the current invention is combined with *in silico* digestion techniques to predict the SNPs that will be present when a genome is digested with a particular enzyme or enzymes and fragments of a particular size are amplified. In Figure 4, a computer is first used to locate a SNP from the public database provided by The SNP Consortium (TSC), (available on the internet at ~~http://snp.cshl.org/~~ snp.cshl.org last visited 7/25/2001) in the public database of the sequence of the human genome, available in GenBank (See, ~~www.ncbi.nlm.nih.gov~~ ncbi.nlm.nih.gov, last visited 7/25/2001). The computer is then used to predict the, for example, *Bgl*III restriction sites upstream and downstream of a given SNP. For example, in Figure 4 TSC SNP ID 10034 has a *Bgl*III site at upstream position 49050 and a downstream *Bgl*III site at position 52100. Given these restriction sites the computer would further predict that SNP 10034 would be contained on a 3050 base pair fragment when genomic DNA was digested with *Bgl*III.